



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number:

TO: Terra Gibbs
Location: CM1/12A12/11E12
Art Unit: 1635
Tuesday, June 24, 2003

Case Serial Number: 998667

From: Mary Jane Ruhl
Location: Biotech-Chem Library
CM1-6A06
Phone: 605-1155

maryjane.ruhl@uspto.gov

Search Notes



From: Gibbs, Terra
Sent: Wednesday, June 18, 2003 12:46 PM
To: "
Subject: STIC-Biotech/ChemLib
Sequence search request...

Could you please do a regular search of SEQ ID NO: 2 of USSN 09/998667?

Thank You!

Terra Gibbs
AU 1635
306-3221
Mailbox: 11E12

ivary Jane Ruhl
Tech. Info. Specialist, STIC
TC-1600
CM-1, Room 6A-06
Phone: 605-1155



score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Run on: June 23, 2003, 10:59:25 ; Search time 5148 Seconds

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Run on:      June 23, 2003, 10:58:25 : Search time 5148 seconds
              (without alignments)
              11481 701 Million cell
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Gap of 1000 : Gap of 1000

Total number of hats satisfying chosen parameters: 41,092,800

Minimum PR seq length: 0
Maximum PR seq length: 2000000000

Post - processing

Listing first 45 summaries

Dattabhar

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part_1 *  
1: gb_ba:*
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3: gb_in: *

7b. 24. 5.

• Uganda •

9: qb_pr: *

11: qb sts -

13: qb un.

em_ba: *

em_hum

em_m11: 13.
em_m11: 13.
em_m11: 13.

2.1. $\Delta m = 0$

2000

24: em_ph: 4

25: em_ro: "

23: em_un: *

30: em_htg_

32: em_htg_

34. em_htg

36: em_htg_

38: em_sy: #

40: em_htgc

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Pred. No. is the number of results predicted by chance to have a

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|---------|----|-----------|---------------------|
| 1 | 1916 | 94.3 | 1516 | q | AB000463 | AB000463 Homo sapi |
| 2 | 1504.6 | 74.3 | 1549 | q | BC013523 | BC013523 Homo sapi |
| 3 | 1396.8 | 68.4 | 1804 | q | AF060918 | AF060918 Macaca fa |
| 4 | 920.8 | 44.4 | 1663.8 | q | AF0609293 | AF0609293 Homo sapi |
| 5 | 920.8 | 44.4 | 1753.3 | q | AF060930 | AF060930 Homo sapi |
| 6 | 920.8 | 44.4 | 1823.2 | q | AF060931 | AF060931 Homo sapi |
| 7 | 654.8 | 32.2 | 1734.03 | q | AF060932 | AF060932 Homo sapi |
| 8 | 335.2 | 11.4 | 1556.67 | q | AF060936 | AF060936 Homo sapi |
| 9 | 282.2 | 11.4 | 1478.63 | q | AF060937 | AF060937 Homo sapi |
| 10 | 230 | 11.3 | 6499.0 | q | AF060938 | AF060938 Homo sapi |
| 11 | 230 | 11.3 | 1035.00 | q | AF060939 | AF060939 Homo sapi |
| 12 | 230 | 11.3 | 1035.00 | q | AF060940 | AF060940 Homo sapi |
| 13 | 230 | 11.3 | 1035.00 | q | AF060941 | AF060941 Homo sapi |
| 14 | 230 | 11.3 | 1400.00 | q | AF060942 | AF060942 Homo sapi |
| 15 | 227.4 | 11.2 | 1685.47 | q | AF060943 | AF060943 Homo sapi |
| 16 | 207.4 | 11.2 | 1631.47 | q | AF060944 | AF060944 Homo sapi |
| 17 | 206.4 | 11.1 | 1393.52 | q | HS0607823 | HS0607823 Homo sapi |
| 18 | 205.4 | 11.1 | 1507.53 | q | AF0607824 | AF0607824 Homo sapi |
| 19 | 204.8 | 11.1 | 1689.37 | q | AF0607825 | AF0607825 Homo sapi |
| 20 | 204.8 | 11.1 | 1837.41 | q | AC073856 | AC073856 Homo sapi |
| 21 | 204.8 | 11.1 | 2013.97 | q | AC073860 | AC073860 Homo sapi |
| 22 | 214 | 11.0 | 943.00 | q | AF0607834 | AF0607834 Homo sapi |
| 23 | 203.4 | 11.0 | 1653.94 | q | AF0607837 | AF0607837 Homo sapi |
| 24 | 203.4 | 11.0 | 1143.06 | q | AF0607838 | AF0607838 Homo sapi |
| 25 | 203.2 | 11.0 | 1243.39 | q | AC0008487 | AC0008487 Homo sapi |
| 26 | 203.2 | 11.0 | 1473.40 | q | AC010526 | AC010526 Homo sapi |
| 27 | 223 | 11.0 | 1468.22 | q | AC010581 | AC010581 Homo sapi |
| 28 | 222.8 | 11.0 | 1356.98 | q | AF0605219 | AF0605219 Homo sapi |
| 29 | 222.8 | 11.0 | 1446.66 | q | AF060587 | AF060587 Homo sapi |
| 30 | 222.8 | 11.0 | 1879.62 | q | AC0007831 | AC0007831 Homo sapi |
| 31 | 202.4 | 11.0 | 1285.68 | q | HS0115403 | HS0115403 Homo sapi |
| 32 | 202.2 | 11.0 | 1334.72 | q | AF061374 | AF061374 Homo sapi |
| 33 | 202.2 | 10.9 | 2481.4 | q | AF050387 | AF050387 Homo sapi |
| 34 | 202.2 | 10.9 | 437.75 | q | AF050388 | AF050388 Homo sapi |
| 35 | 202.2 | 10.9 | 197.72 | q | AF0507511 | AF0507511 Homo sapi |
| 36 | 202.2 | 10.9 | 2018.21 | q | AC0129105 | AC0129105 Homo sapi |
| 37 | 202.2 | 10.9 | 1496.42 | q | AC0118721 | AC0118721 Homo sapi |
| 38 | 202.2 | 10.9 | 1514.33 | q | AF0606761 | AF0606761 Homo sapi |
| 39 | 202.2 | 10.9 | 1604.96 | q | AC0034708 | AC0034708 Homo sapi |
| 40 | 222 | 10.9 | 1673.37 | q | AC012903 | AC012903 Homo sapi |
| 41 | 221.6 | 10.9 | 1543.88 | q | AF051364 | AF051364 Homo sapi |
| 42 | 221.6 | 10.9 | 908.88 | q | AF051385 | AF051385 Homo sapi |
| 43 | 221.6 | 10.9 | 1348.26 | q | AF050910 | AF050910 Homo sapi |
| 44 | 221.6 | 10.9 | 1543.77 | q | AF050911 | AF050911 Homo sapi |
| 45 | 221.4 | 10.9 | 1742.31 | q | AF051354 | AF051354 Homo sapi |

ALIGNMENTS

| | |
|------------|----------------------------------------------------------------------------------------------------------------------------------|
| RESULT | AK000463 |
| LOCUS | AK000463 |
| DEFINITION | Homo sapiens CDNA FLJ20456 fis, clone KAT05827. |
| ACCESSION | AK000463 |
| VERSION | AY000463.1 (31-7070568) |
| KEYWORDS | oligo capping; fis (full insert sequence). |
| SOURCE | Homo sapiens sigmoid ring cell carcinoma cell_line KAT 111 cDNA library. Clone ID: KAT05827. |
| ORGANISM | Homo sapiens |
| REFERENCE | Eukaryotic Metazoa; Chordata; Cetartia; Vertebrata; Artelocetia; Mammalia; Eutheria; Primates; Carnarhin; Homindae; Homo. |
| AUTHORS | Maratbaev K., Kumagai A., Itakura S., Yamashita M., Tsiang G.H., J. Li, Suzuki Y., Shibasaki M., Nishida S., Okabe M., Tanaka T. |

[illegible]

| | | | | | |
|-------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|-------------|------|---------|-----------------|
| RESULT: | BC010021 | 1549 bp | mpna | library | pg: 02.AUG.2001 |
| LOCUS: | | | | | |
| DEFINITION: | Homo sapiens, clone M3C 21737 IMAGE.451247, mRNA, complete cds. | | | | |
| ACCESSION: | BC010021 | | | | |
| VERSION: | BC010021.1 | GI:15080561 | | | |
| KEYWORDS: | M3C | | | | |
| SOURCE: | Homo sapiens. | | | | |
| ORGANISM: | Homo sapiens. | | | | |
| REFERENCE: | Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo
1 (bases 1 to 1549); | | | | |

JOINTLY: September 13, 2001: National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-7560, USA
NIG MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk

DNA Library Arrayed by The I.M.A.G.E. Consortium (IHL)
 Data Generated by Raytek Collig of Medvetec Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/Cdna4>
 Contact: vc@hsc.tmc.edu
 Villalon, D.F., Luna, P.A., Reile, S.M., Rilyk, S., Lu, X., Garcia,
 A.M., Holmwood, M., Telford, R., Holmwood, A., Boucek, J., Yu, W.,
 Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E Consortium at <http://img.jgi.gov/SerVICES/IPAF/PlateID8Pow3/Column11>. This clone was sequenced by the JGI sequencing facility and passed the following sequence criteria. Genomic gene prediction.

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# Features
# ...
Location/Qualifiers
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/db_xref "taxon:9606"
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MIM:1173 IMAGE_4501247
/tissue_type "testis; embryonal carcinoma"
/clone_lib="NH_MGC_92"

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/ab host="TH10B"
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14. 712
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/translation="MSGSLSTDGSKAPASATARAERRRDEPDELVTITDAAVETVY
LHVPATPAHVPSPATATKPNPWYFAVQVAVTAAVQEVYVNE
CDVYLSEEMAHITDQYIEVLEKLEETATAPVETDRIYVSLLEITIT
HSEKPPVPLCELEPENSSTFLLPHEVSETPVETENIEVVALPQV
DRLLEYVNSHTA"
BASE COUNT      464 a      213 c      370 g      402 t
ORIGIN
      74 aa      score 1594.6      DP 3      length 104
Query Match      99.4%      Eexp No. 0
Matches 1523: Conservative      0: Mismatches      14: Indels      0: gaps

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[illegible]

| | | |
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| 1 | 1033 | contig of 1033 bp in length |
| 1034 | 1133 | gap of 100 bp |
| 1134 | 5795 | contig of 4662 bp in length |
| 5796 | 5895 | gap of 100 bp |
| 5896 | 10385 | contig of 4491 bp in length |
| 10387 | 10486 | gap of 100 bp |
| 10487 | 15318 | contig of 4832 bp in length |
| 15319 | 15418 | gap of 100 bp |
| 15419 | 19106 | contig of 3688 bp in length |
| 19107 | 19255 | gap of 100 bp |
| 19207 | 26260 | contig of 6414 bp in length |
| 25621 | 25720 | gap of 100 bp |
| 25721 | 31795 | contig of 6075 bp in length |
| 31796 | 31925 | gap of 100 bp |
| 31986 | 38072 | contig of 6177 bp in length |
| 38073 | 38178 | gap of 100 bp |
| 38179 | 47433 | contig of 9261 bp in length |
| 47444 | 47533 | gap of 100 bp |
| 47534 | 54692 | contig of 7159 bp in length |
| 54693 | 54702 | gap of 100 bp |
| 54793 | 66099 | contig of 14277 bp in length |
| 66099 | 67132 | gap of 100 bp |
| 67170 | 828605 | contig of 18336 bp in length |
| 82866 | 82706 | gap of 100 bp |
| 82706 | 94840 | contig of 13185 bp in length |
| 94841 | 94841 | gap of 100 bp |
| 95991 | 106707 | contig of 10717 bp in length |
| 106708 | 106807 | gap of 100 bp |
| 106808 | 128545 | contig of 17738 bp in length |
| 124506 | 124545 | gap of 100 bp |
| 124546 | 166218 | contig of 41573 bp in length |

```

/organism: "Homo sapiens"
/db_xref="taxon:9606"

```

```
misc_feature      /close="FP11_5316"  
                  /close_1lb="RPCT-11 Human Male BAC  
1..1033  
/note="assembly_fragment"  
1134..5795  
/note="assembly_fragment"  
5896..10386  
/note="assembly_fragment"  
10487..15318  
/note="assembly_fragment"  
15419..19106  
/note="assembly_fragment  
clone_and_spe  
vector_side:right"  
19207..195620  
/note="assembly_fragment"  
25721..31735  
/note="assembly_fragment"  
31896..138072  
/note="assembly_fragment"  
38173..47433  
/note="assembly_fragment"  
47534..54692  
/note="assembly_fragment"  
54793..69063  
/note="assembly_fragment"  
69174..74715  
/note="assembly_fragment"  
92136..133945  
/note="assembly_fragment"
```

```
misc_feature      95991..106707
                  /note="assembly_fragment"
misc_feature      106808..124545
                  /note="assembly_fragment"
misc_feature      124646..166218
                  /note="assembly_fragment"
                  clone end:77
                  vector side:left"
BASE COUNT      56671 a 32925 c 33721 g 47298 t 1503 otherc
ORIGIN
```

| | Query Match | 95.41% | Score 900.88 | DB 2 | length 166218 | |
|-----|----------------------------------------------------------------|----------------|---------------|----------|---------------|------|
| | Best Local Similarity | 95.71% | Prod No 36703 | | | |
| | Matches 926 | Conservative 0 | Mismatches 42 | Indels 0 | Gaps 0 | |
| 27 | 1664 AACACATCTGCAGGTAGTACGACTTCTTTCTTCTGATCTATATGATATATATATAT | | | | | 1123 |
| DB | 69417 AATACATATGACTCGAATATTTCAATTTATTTCTTATATGTAGATTTTAAATATAT | | | | | 6947 |
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| 100 | | | | | | |


```

repeat_region
      /rpt_family="MIR"
      /rpt_family="MIR"
      complement(8993..9305)
      /rpt_family="AluJo"
repeat_region
      /rpt_family="AT_rich"
      9306..9330
      9512..9547
      /rpt_family="L2"
      complement(9549..9686)
      /rpt_family="FLAM_C"
repeat_region
      9687..9961
      /rpt_family="L2"
      9999..10361
      /rpt_family="AluSq"
      complement(10343..10651)
      /rpt_family="AluSc"
      10373..10387
      /note="<30 qual SNCL region"
      10388..10411
      /note="<30 qual SNCL region"
      10877..11173
      /rpt_family="AluSg"
      11744..12047
      /rpt_family="AluSp"
      12155..12443
      /rpt_family="AluJb"
      complement(12756..13055)
      /rpt_family="AluSg"
      complement(13445..13583)
      /rpt_family="L2"
      13678..13981
      /rpt_family="AluJo"
      complement(14037..14344)
      /rpt_family="THEIC"
      14367..14662
      /rpt_family="AluSp"
      14664..14668
      /rpt_family="AT_rich"
      14987..15225
      /rpt_family="AluSp"
      complement(15744..15988)
      /rpt_family="L3"
      complement(15989..16289)
      /rpt_family="AluSp"
      16290..16430
      /rpt_family="L3"
      16431..16435
      /rpt_family="MERSA"
      16641..16806
      /rpt_family="FRAM"
      complement(16847..17006)
      /rpt_family="L1MA3"
      complement(17007..17236)
      /rpt_family="AluSx"
      complement(17237..18443)
      /rpt_family="L1MA3"
      18444..19076
      /rpt_family="FLAM_A"
      complement(19689..19976)
      19998..20100
      /rpt_family="L2"
      20101..20376
      /rpt_family="L2"
      complement(20598..20658)
      /rpt_family="L2"

```

| | | | | |
|-----------------------|--------------|-----------------|----------------|----------------|
| Query Match | 44.48, | Score 900.8, | DB 0, | Length 176222; |
| Best Local Similarity | 95.78, | Prot No 2e 203, | | |
| Matches 326, | Conservative | 0, | Mismatches 42, | Indels 5, |
| | | | Gaps | 0. |

1004 AAGAAATCTGACCAATTATTAATCAATCCCATGACATTTTAAATAAT 1122

[illegible]

| | |
|------------|------------------------------------------------------------------|
| RESULT 6 | |
| AC036167/c | 183,128 bp |
| GENUS | RNA |
| DEFINITION | 1 linear: HTS 26 JUN 2000 |
| SEQUENCE | How sapiens chromosome 18 clone RP11 592123 map 18. WPKING DPART |
| | SEQUENCE. 43 uncloned pieces. |

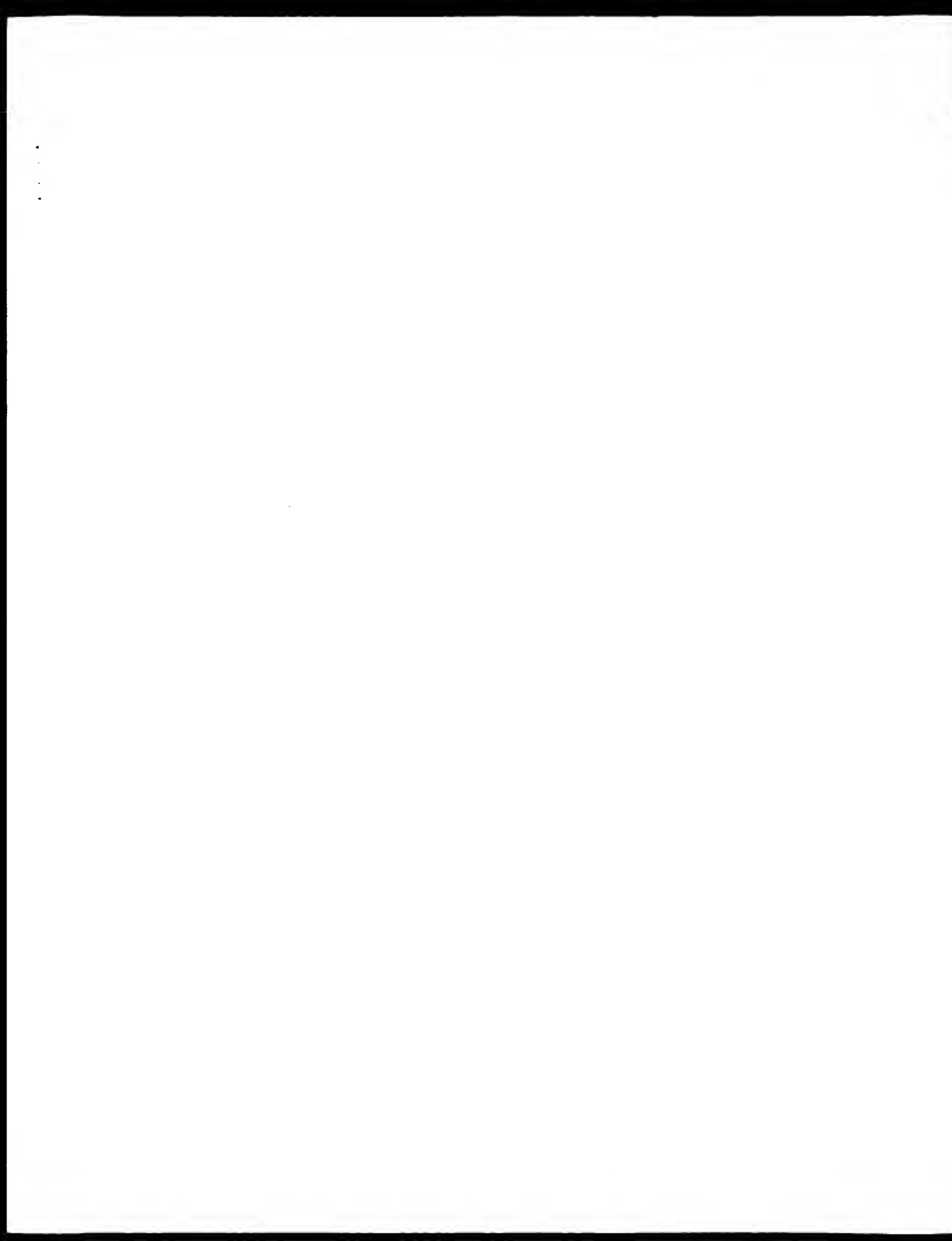
[illegible][illegible]


```

source
  /chromosome="21"
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /chromosome="21"
  /map="21q22.1"
  /clone="R289H18, 5' partial"
  /clone.lib="RP1-11 BAC library"
  /note="Accession No. AP000248"
  64224, 78771
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  /map="21q22.1"
  /clone="R762015"
  /clone.lib="RP1-11 BAC library"
  /note="Accession No. AP000249"
  78691, 147271
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  /map="21q22.1"
  /clone="R0899"
  /clone.lib="RP1 PAC library"
  /note="Accession No. AP000563"
  147007, 164323
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  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /chromosome="21"
  /map="21q22.1"
  /clone="PT1040"
  /clone.lib="CMP21 P1 library"
  /note="Accession No. AP000250"
  159131, 224372
source
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  /db_xref="taxon:9606"
  /chromosome="21"
  /map="21q22.1"
  /clone="PS158"
  /clone.lib="CMP21 P1 library"
  /note="Accession No. AP000251"
  224164, 2291172
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  /db_xref="taxon:9606"
  /chromosome="21"
  /map="21q22.1"
  /clone="PT650"
  /clone.lib="CMP21 P1 library"
  /note="Accession No. AP000252"
  285247, 307588
source
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /chromosome="21"
  /map="21q22.1"
  /clone="PS552"
  /clone.lib="CMP21 P1 library"
  /note="Accession No. AP000253"
  303103, 333859
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  /db_xref="taxon:9606"
  /chromosome="21"
  /map="21q22.1"
  /clone="R6312"
  /clone.lib="CMP21 P1 library"
  /note="Accession No. AP000254"
  331793, 340000
source
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /chromosome="21"
  /map="21q22.1"
  /clone="H111398, 3' partial"
  /clone.lib="CMP21 P1 library"
  /note="Accession No. AF000255"

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| Query Match | Best Local Similarity | 80.9% | Fred No. 1.7e-43 | Matches 283 | Conservative 0 | Mismatch 60 | Indels 7 | Gaps 1 |
|---------------|-----------------------|----------------|------------------------------|--------------------|----------------|-------------|-----------------------|--------------------|
| repeat_region | 1172..1287 | /note="LTR16a" | /rpt_family="LTR/retroviral" | /rpt_type=DISPERSD | 1397..2428 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 1397..2428 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 2535..3287 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 2535..3287 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 2828..3294 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 2828..3294 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 2925..3267 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 2925..3267 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 3293..3322 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 3293..3322 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 3719..4343 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 3719..4343 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 4860..4907 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 4860..4907 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 5034..5199 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 5034..5199 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 5468..5502 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 5468..5502 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 5504..5598 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 5504..5598 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 5599..5693 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 5599..5693 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 5694..5788 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 5694..5788 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 5789..5883 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 5789..5883 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 5884..5978 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 5884..5978 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 5979..6073 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 5979..6073 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 6074..6168 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 6074..6168 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 6169..6263 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 6169..6263 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 6264..6358 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 6264..6358 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 6359..6453 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 6359..6453 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 6454..6548 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 6454..6548 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 6549..6643 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 6549..6643 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 6644..6738 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 6644..6738 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 6739..6833 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 6739..6833 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 6834..6928 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 6834..6928 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 6929..7023 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 6929..7023 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 7024..7118 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 7024..7118 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 7119..7213 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 7119..7213 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 7214..7308 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 7214..7308 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 7309..7403 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 7309..7403 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 7404..7498 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 7404..7498 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 7499..7593 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 7499..7593 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 7594..7688 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 7594..7688 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD | 7689..7783 | /note="L2" | /rpt_family="LINE/L2" | /rpt_type=DISPERSD |
| repeat_region | 7689..7783 | /note="L2" | /rpt_family="LINE/L2" | | | | | |



GenCore version 5.1.6
Copyright (c) 1993 2003 CompuGen Ltd.

GM nucleotide search, using SW model

Run on: June 23, 2003, 08:48:15, Search time 464 Seconds
(without alignments)

9857346 Million cell updates/sec

Time: 09-998-667-2

Perfect score: 1.0333333333333333

Sequence: 1.0333333333333333

Sequence: 1.0333333333333333

Identified: 238994 sequences

Total number of hits satisfying chosen parameters: 4370478

Minimum hit seq length: 0
Maximum hit seq length: 20000000

First alignment: Maximum Match 100%

Listing first 45 summaries

Database:

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1. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1989.DAT *
2. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1981.DAT *
3. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1982.DAT *
4. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1983.DAT *
5. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1984.DAT *
6. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1985.DAT *
7. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1986.DAT *
8. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1987.DAT *
9. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1988.DAT *
10. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1989.DAT *
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12. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1991.DAT *
13. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1992.DAT *
14. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1993.DAT *
15. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1994.DAT *
16. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1995.DAT *
17. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1996.DAT *
18. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1997.DAT *
19. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1998.DAT *
20. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA1999.DAT *
21. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA2000.DAT *
22. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA2001.DAT *
23. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA2002.DAT *
24. /SIDS2/3cgdata/geneseq/geneseq-emb1/NA2003.DAT *
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB ID | Description |
|------------|--------|-------|--------------|-------|----------------------|
| 1 | 1037.6 | 51.1 | 1236 | 22 | Human polynucleotide |
| 2 | 573.2 | 28.2 | 588 | 22 | Human polynucleotide |
| 3 | 518.2 | 25.6 | 1016 | 22 | Human immune system |
| 4 | 457.4 | 22.6 | 468 | 21 | Human CPX CP162 |
| 5 | 320 | 10.8 | 267156 | 24 | Human nervous system |
| 6 | 219.2 | 10.8 | 8197 | 22 | Human immune system |
| 7 | 219.2 | 10.8 | 8568 | 22 | Human immune system |
| 8 | 219.2 | 10.8 | 8568 | 24 | Human immune system |
| 9 | 219.2 | 10.8 | 8568 | 24 | Human immune system |

ALIGNMENTS

| | | | | | |
|----|-------|------|------|----|---------------------|
| 10 | 219.2 | 10.8 | 8568 | 24 | Human immune system |
| 11 | 218.2 | 10.7 | 368 | 21 | Human immune system |
| 12 | 218.2 | 10.7 | 368 | 21 | Human immune system |
| 13 | 217 | 10.7 | 368 | 21 | Human immune system |
| 14 | 216.6 | 10.7 | 1548 | 22 | Human immune system |
| 15 | 216.2 | 10.6 | 333 | 22 | Human immune system |
| 16 | 216.2 | 10.6 | 333 | 22 | Human immune system |
| 17 | 216.2 | 10.6 | 333 | 22 | Human immune system |
| 18 | 215.8 | 10.6 | 333 | 22 | Human immune system |
| 19 | 215.8 | 10.6 | 333 | 22 | Human immune system |
| 20 | 215.8 | 10.6 | 333 | 22 | Human immune system |
| 21 | 215.8 | 10.6 | 333 | 22 | Human immune system |
| 22 | 215.8 | 10.6 | 333 | 22 | Human immune system |
| 23 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 24 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 25 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 26 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 27 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 28 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 29 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 30 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 31 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 32 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 33 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 34 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 35 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 36 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 37 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 38 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 39 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 40 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 41 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 42 | 214.8 | 10.6 | 333 | 22 | Human immune system |
| 43 | 214.8 | 10.6 | 333 | 22 | Human immune system |
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[illegible]

03-OCT-2000; 2200US-237608P.
PE 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
RE 01-NOV-2000; 2000US-245084P.

(AVALON PHARM.)
XX XX
PA Young PE, Augustus M., Carter KC, Ehrner R., Endress G., Horrigan S,
XX XX P1 Soppe DR, Weaver Z;
DR WPI: 2002-198264/24.
XX XX
PT Screening for anti-neoplastic agent involves exposing cells to a
FT chemical agent to be tested for anti-neoplastic activity, and
RT determining a change in expression of a gene of a signature gene set -
PS Claim 1; SEQ ID 1247; 44pp, English.

The present invention describes a method (W) for screening for anti-neoplastic agents. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from said signatures listed in Affected ABL7011(1), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has neoplastic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, adenocarcinoma, glioblastoma, kidney, prostate or pancreatic cancer, carcinomas, carcinoma, clear cell cancer, infiltrating ductal carcinoma, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumor.

SEQ Sequence 45608 PP: 15447 A; 16479 C; 16761 G; 16978 T; 3 other;

Query Match 10.9%, Score 219.2, DP 24, Length 656/681;
Best Local Similarity 80.8%, Read HQ: 9e-45;
Matches 271; Conservative 0; Mismatches 58; Indels 7; Gaps 1;

DY AAAATTTGAAAGTCAAAAAGGTATTTCACCAAGAAGCAGCGGGTAACGAGTGAATG 1745
DB AAATAAAAAAAAAAAAAAAAGAACAAACAATTTTGAGTCCCATGAGTGCAGTAAAT 4376

DY AACACTATTGCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 1819
DB AGAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGT 4376

DY GTTAAATATGATGTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1875
DB GTTAAATATGATGTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 4388

DY GTTAAATATGATGTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1919
DB GTTAAATATGATGTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 4444

DY GTTAAATATGATGTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2011
DB GTTAAATATGATGTTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 4444

DY AACCAAAATGACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 4456
DB AACCAAAATGACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 4456

RESULT 9
ABU64414
ID ABU64414 standard, DNA, 65608 BP.
XX ABU64414,
XX



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| 27 | 1833 | GTGAAATTTTCTTATCTGAAAAAG-AAAAGTTGCTGAAATCTTTGAGGAGATCTG | 1896 |
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| 26 | 2697 | GTGAAATTTTCTTATCTGAAAAATTAATAAAATTAATTTGCTTATCTGAGGAGATCTG | 148 |
| | | | |
| 25 | 1891 | GTATATCAATTAATCTGAGAGCTTAAGATTAAGAGATTAATTAATTAAGAGATTAATCT | 1950 |
| | | | |
| 24 | 147 | TATCTGAGATTTGAGAGCTTAAGATTAAGAGATTAATTAATTAAGAGATTAATCT | 88 |
| | | | |
| 23 | 1951 | TGATGAGATTAATCTGAGAGCTTAAGATTAAGAGATTAATTAATTAAGAGATTAATCT | 2010 |
| | | | |
| 22 | 87 | TGATGAGATTAATCTGAGAGCTTAAGATTAAGAGATTAATTAATTAAGAGATTAATCT | 28 |
| | | | |
| 21 | 2011 | TCGAAAAAAAAAAAAAAAAAAAAA | 2031 |
| | | | |
| 20 | 27 | TCGAAAAAAAAAAAAAAAAAAAAA | 7 |

RESULT 7
US-09-033-333-3/c
; Sequence 3, Application US/090333333
; Patent NO 6197293

GENERAL INFORMATION:
APPLICANT: Yu, De Chao
APPLICANT: Schuur, Eric
TITLE OF INVENTION: HENDERSON, Daniel
TITLE OF INVENTION: ALEVINIPIS VENTURES SPECIFIC
TITLE OF INVENTION: FOR TILLS EXISTING AND OTHER INVENTIONS AND METHODS
TITLE OF INVENTION: THREEOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,333
FILING DATE: 02-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,110
REFERENCE/DOCKET NUMBER: 1400, 0000, 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-814-5600
TELEFAX: 650-494 0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5835 base pairs
type: nucleic acid

| US-09-033-333-3 | TELELOGY | Linear |
|---------------------------|-------------------|---------------------------------|
| Query Match | 10 2% | Score 207.3; pp 4; length 5825; |
| Best Local Similarity | At 4% | Find No. 3,4e-44; |
| Matches 252; Conservative | 0; Mismatches 48; | Indels 6; Gaps 1 |

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GenCore version 5.1.6
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Run on: June 23, 2003, 13:32:34, Search time 293 Seconds
 (without alignments)
 10171,825 Million cell updates/sec

Target: US-09-998-667-2
 Product score: 100
 Sequence: 100
 Identity: 100
 Gap: 100

Sequenced: 1642519 bytes, 73371590 residues

Total number of hits satisfying chosen parameters: 2086018

Minimum DB seq length: 0

Maximum DB seq length: 300000000

Post processing: Maximum Match: 28
 Maximum Match: 100%

Listing first 45 summaries

Database: Published Applications NA:

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 2. /cgn2_6/prodara/1/publpa/PCOM_NEW_PUB seq.*
 3. /cgn2_6/prodara/1/publpa/PCOM_NEW_PUB seq.*
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 10. /cgn2_6/prodara/1/publpa/US08_PUBCOMB seq.*
 11. /cgn2_6/prodara/1/publpa/US08_PUBCOMB seq.*
 12. /cgn2_6/prodara/1/publpa/US08_PUBCOMB seq.*
 13. /cgn2_6/prodara/1/publpa/US08_PUBCOMB seq.*
 14. /cgn2_6/prodara/1/publpa/US08_PUBCOMB seq.*

Prod No is the number of results prefiltered by change to have a score greater than or equal to the score of the result being printed, and is derived by analyzing the results of the distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 2031 | 100.0 | 2031 | 10 | US-09-998-667-2 |
| 2 | 1836.4 | 99.9 | 4444 | 10 | US-09-998-667-2 |
| 3 | 1620 | 99.8 | 1620 | 10 | US-09-998-667-2 |
| 4 | 1037.6 | 91.1 | 1236 | 9 | US-10-017-270-1077 |
| 5 | 765 | 17.7 | 765 | 10 | US-09-998-667-2 |
| 6 | 709.4 | 14.4 | 1404 | 10 | US-09-998-667-2 |
| 7 | 519.2 | 25.5 | 1015 | 9 | US-09-949-842-7 |
| 8 | 220 | 10.8 | 684973 | 10 | US-09-263-959-1 |
| 9 | 219.2 | 10.8 | 65664 | 10 | US-09-263-959-1 |
| 10 | 219.2 | 10.8 | 65664 | 10 | US-09-263-959-1 |
| 11 | 219.2 | 10.8 | 65664 | 10 | US-09-263-959-1 |
| 12 | 217 | 10.7 | 7566 | 9 | US-09-764-891-11010 |
| 13 | 215.2 | 10.6 | 16284 | 9 | US-09-764-891-11010 |
| 14 | 214.8 | 10.5 | 31474 | 9 | US-09-764-891-11010 |
| 15 | 214.2 | 10.5 | 27154 | 9 | US-09-764-891-11010 |
| 16 | 214 | 10.5 | 1701 | 9 | US-09-728-552-9 |
| 17 | 213 | 10.5 | 6437 | 10 | US-09-764-891-11010 |
| 18 | 213 | 10.5 | 16086 | 10 | US-09-764-891-11010 |
| 19 | 213 | 10.5 | 169114 | 9 | US-10-067-514-1 |

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|----|-------|------|--------|----|---------------------|
| 20 | 212.4 | 10.5 | 3407 | 9 | US-09-764-891-11010 |
| 21 | 211.6 | 10.4 | 2829 | 9 | US-10-116-255-15 |
| 22 | 211.6 | 10.4 | 5131 | 9 | US-10-116-255-15 |
| 23 | 211.6 | 10.4 | 5131 | 9 | US-10-116-255-15 |
| 24 | 211.6 | 10.4 | 5131 | 9 | US-10-116-255-15 |
| 25 | 211.6 | 10.4 | 5131 | 9 | US-10-116-255-15 |
| 26 | 211.6 | 10.4 | 5131 | 9 | US-10-116-255-15 |
| 27 | 211.2 | 10.4 | 23748 | 9 | US-09-764-891-11010 |
| 28 | 211.2 | 10.4 | 16892 | 9 | US-09-764-891-11010 |
| 29 | 211 | 10.4 | 63000 | 10 | US-09-780-172-18 |
| 30 | 210.4 | 10.4 | 337 | 10 | US-09-764-891-11010 |
| 31 | 210.4 | 10.4 | 14332 | 10 | US-09-764-891-11010 |
| 32 | 210.4 | 10.4 | 14092 | 10 | US-09-764-891-11010 |
| 33 | 210.4 | 10.4 | 14092 | 10 | US-09-764-891-11010 |
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| 35 | 210.4 | 10.4 | 14092 | 10 | US-09-764-891-11010 |
| 36 | 210.2 | 10.3 | 15714 | 10 | US-09-764-891-11010 |
| 37 | 210 | 10.3 | 714 | 10 | US-09-764-891-11010 |
| 38 | 210 | 10.3 | 714 | 10 | US-09-764-891-11010 |
| 39 | 210 | 10.3 | 714 | 10 | US-09-764-891-11010 |
| 40 | 210 | 10.3 | 14092 | 10 | US-09-764-891-11010 |
| 41 | 210 | 10.3 | 11360 | 9 | US-09-764-891-11010 |
| 42 | 210 | 10.3 | 11360 | 9 | US-09-764-891-11010 |
| 43 | 210 | 10.3 | 11360 | 9 | US-09-764-891-11010 |
| 44 | 210 | 10.3 | 28497 | 10 | US-09-764-891-11010 |
| 45 | 210 | 10.3 | 684972 | 10 | US-09-764-891-11010 |

ALIGNMENTS

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| 2 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
| 3 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
| 4 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
| 5 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
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| 7 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
| 8 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
| 9 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
| 10 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
| 11 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
| 12 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
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| 14 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
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| 16 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
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| 18 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
| 19 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
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| 21 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
| 22 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
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| 25 | US-09-998-667-2 | Sequence 1, Appl 1 | Sequence 1, Appl 1 |
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```

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun
APPLICANT: Chen, Kai-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Whitman, Tom
APPLICANT: Xue, Aizong J.
APPLICANT: Yu, Yushu J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Junqing
APPLICANT: Wang, Dunwei
APPLICANT: Wang, Zhwei
APPLICANT: Tillinghast, John
APPLICANT: Demanac, Radcoje T.
TITLE OF INVENTION: New methods for detecting and
FILER REFERENCE: 78412B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ. ID NOS: 1104
SOFTWARE: JF Fasta Version 1.0
SEQ. ID NO 1077
LENGTH: 1236
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: JTS
LOCATION: (111) (809)
NAME/KEY: m100 Fasta
LOCATION: (11) (11236)
OTHER INFORMATION: n = 4.1e-04 g
US: 10-998-270 1077

Query Match          51.1%, Score 1037.6; DB 9; Length 1236;
Best Local Similarity 99.6%, P-adj No 1.5e-278;
Matches 1040; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Query 5
US-09-998-667-4
Sequence 4, Application US/09-998-667
Patent No. US20020146747A1
GENERAL INFORMATION:
APPLICANT: Masuda, Esteban
APPLICANT: Liao, X. Charlene
APPLICANT: Zhao, Haoran
APPLICANT: Chu, Peter
APPLICANT: Pardo, Jorge
APPLICANT: Pardo, Jorge
TITLE OF INVENTION: Tract, Molecular
TITLE OF INVENTION: Tract, Molecular
FILER REFERENCE: 021044-000600US
CURRENT APPLICATION NUMBER: 09/049,467
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 09/242,432
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ. ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ. ID NO 4
LENGTH: 765
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: JTS
LOCATION: (111) (809)
NAME/KEY: m100 Fasta
LOCATION: (11) (11236)
OTHER INFORMATION: n = 4.1e-04 g
US-09-998-667-4
Query Match          37.7%, Score 765; DB 10; Length 765;

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QY 1996 GAGTAACTCTGATCCGAAAAA 2031
 DB 45501 AAGTAAAGTCTCTGATCCGAAAAA 43536

RESULT 11

US-09-962-832-119
 Sequence 119, Application US/09962832
 Patent No. 6820201/9621A

GENERAL INFORMATION:

APPLICANT: Ebel, Reinhard
 TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
 FILE REFERENCE: 689290-74
 CURRENT AFFILIATION NUMBER: US/09-962-832
 CURRENT FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US/09-962-832
 PRIOR FILING DATE: 2000-09-25
 PRIOR APPLICATION NUMBER: US/09-962-832
 PRIOR FILING DATE: 2000-09-25
 NUMBER OF SEQ. ID NOS: 259
 SOFTWARE: PatentIn version 3.0
 SEQ. ID NO: 119
 LENGTH: 65608
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURES:
 NAME/KEY: misc feature
 OTHER INFORMATION: n=4, t=3 or 2
 US-09-962-832-119

Query Match 10.8%, Score 219.2, DB 10, Length 65608;
 Best Local Similarity 80.7%, Pred. No. 3, Re-49;
 Matches 271, Conservative 0, Mismatches 58, Indels 7, Gaps 1;

QY 1696 AAAATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1755
 DB 41208 AAAAAAAGAAAAAAGAAAAAGAAAGAAATTTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 43267
 QY 1756 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1815
 DB 41268 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 43327
 QY 1815 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1875
 DB 41328 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 43387
 QY 1875 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1935
 DB 41388 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 43447
 QY 1935 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1995
 DB 41448 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 43507
 QY 1995 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 2031
 DB 41501 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 43560

RESULT 12

US-09-764-891-10010
 Sequence 10010, Application US/09764891
 Publication No. US6030377/898A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: P0006
 CURRENT APPLICATION NUMBER: US/09/764,891
 CURRENT FILING DATE: 2001-01-17
 Prior application data removed - consult PALM or file wrapper
 NUMBER of SEQ. ID NOS: 10231

SOFTWARE: PatentIn Ver. 2.0
 SEQ. ID NO: 10010
 LENGTH: 7566
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-764-891-10010

Query Match 10.7%, Score 217, DB 2, Length 7566;
 Best Local Similarity 82.2%, Pred. No. 2, Re-49;
 Matches 264, Conservative 0, Mismatches 11, Indels 7, Gaps 1;

QY 1711 AAAAAAGTCAATTTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1771
 DB 467 AAAAAAGTCAATTTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1831
 QY 1771 GGTGAGCGGAGCGGTGAGCTTACGCTTGTAGTC 1831
 DB 427 GGTGAGCGGAGCGGTGAGCTTACGCTTGTAGTC 1891
 QY 1831 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1891
 DB 480 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 439
 QY 1891 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1951
 DB 440 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 499
 QY 1951 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 2011
 DB 500 TATGATTTTCTCAAGTCAAGAAAGTCAATTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 559
 QY 2011 TCAAAAAAAGAAAAAAGAAAAA 2031
 DB 560 TCAAAAAAAGAAAAAAGAAAAA 580

RESULT 13
 US-09-938-795A-3/C
 Sequence 3, Application US/09938795A
 Publication No. US20030045688A1
 GENERAL INFORMATION:
 APPLICANT: CHU, CHARLES CHIYUAN
 APPLICANT: CHAVAN, SANGEETA S
 TITLE OF INVENTION: HUMAN INTERLEUKIN 10B INHIBITORY PROTEIN
 FILE REFERENCE: LIT-9000-US
 CURRENT AFFILIATION NUMBER: US/09-938-795A
 CURRENT FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: US/09-938-795A
 PRIOR FILING DATE: 2000-08-25
 NUMBER OF SEQ. ID NOS: 29
 SOFTWARE: PatentIn Ver. 2.1
 SEQ. ID NO: 3
 LENGTH: 10283
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-938-795A-3

Query Match 10.6%, Score 215.2, DB 9, Length 10283;
 Best Local Similarity 82.9%, Pred. No. 1, Re-48;
 Matches 272, Conservative 0, Mismatches 48, Indels 8, Gaps 2;

QY 1704 GAAAGTCAATTTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1763
 DB 4136 GAAAGTCAATTTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 4077
 QY 1763 GAAAGTCAATTTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1823
 DB 4076 GAAAGTCAATTTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 4017
 QY 1823 GAAAGTCAATTTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 1883
 DB 4016 GAAAGTCAATTTAGGCGGAGCGGTGAGCTTACGCTTGTAGTC 4004

[illegible]

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| | RESULT | 1 |
| | LOCUS | BM469263 |
| | DEFINITION | BM469263 Homo sapiens mRNA for IWRG-546785 |
| | VERSION | BM469263.1 |
| | KEYWORDS | EST. |
| | SOURCE | Homo sapiens |

REFERENCE 1 (bases 1 to 1046)

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT: Contact Robert Strassberg, PhD

Tissue Procurement. A700

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

Clone distribution. MCC clone distribution can be

http://image1.mt.com

High quality sequence coverage: 41%.

HEALING
SOUND
1. 1046
1047/Qualifiers

```

/organdis="HOMINO sapiens"
/abv="38CT 9606"

```

```
/clone --image=5585195  
/clone --p="N1H M2C 92"
```

```
/tissue_type="embryonal carcinoma, cell line"  
/lab_host="DH10B (phage-resistant)"
```

```

/note="Organ: testis; Vector: pCMV-SPOK16; site_1: NotI;
Site 2: SalI; cloned unidirectionally; 0190-dT-primed

```

Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies

Note: this is a NIH_MGC Library."

ORIGIN

| Query Match | Score | DB | Length |
|-------------|--------|--------|--------|
| 31.98; | 648.4; | DB 13; | 1046; |

Matches 73, Conservation 6, Mismatches 101, Indels 12, Gaps 7,

490 GCACAGTGAATGAGGTTGGTGTGAGGCACTGAGCAATGAGGTTGGTGTGTA 549

100 5 GGAATGATGATTCTGTAAGAAAGGAGGAAATGGGGGCGGCTCTGGCA 65

609
GCTTGGACTGCC

66 CCGCGCGCTTTGAGGCTAGAGGAGGAGCGGCGAGTTGCTTGTAAGTCTTGACTGCG 125

[illegible][illegible]


```

/science_id "NCI_OGAP Mam3"
/tissue_type="tumor, gross tissue"

```


| | | | | |
|-------------|-------|--------|--------------|--------------------|
| BASE COUNT | 246 A | 180 C | 132 G | 238 T |
| ORIGIN | | | | |
| Query Match | | 12.7%; | score 398.4; | EB 13; Length 956; |

| | |
|--------------|--------------|
| DECK | 91.104107006 |
| EST. | |
| KEYWORDS | |
| STIFFCE | |
| house mouse. | |

Plate: L1AM13559 row: d column: 13
 High quality sequence start: 14
 High quality sequence stop: 538.
 Location/Qualifiers

FEATURES

source

1..985
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="IMAGE:6178908"
 /sex="male"
 /issue_type="dorsal root ganglia"
 /dev_stage="adult, 36 yr"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site_2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCACACCAACAGCTCC-3' and
 5'-GACTAGTTCTAGATCGGAGCGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.7 kb. This is a primary
 library, non-amplified library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."

BASE COUNT 239 a 232 c 206 g 248 t
 ORIGIN

Query Match 16.8%; Score 341.8; DB 14; Length 985;
 Best Local Similarity 98.0%; Pred No. 6 ea-50;
 Matches 346; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

767 CAAAGAAATTAATCAAGTATTAAGAAATGCGCTGAGTGAACCCCTGTTGGCTCG 826
 7 CCAATATATGAAATCAAGTATTAAGAAATGCGCTGAGTGAACCCCTGTTGGCTCG 66
 827 TGAATATGAGGCAATATTTGGAATCTTTCAGAAATGATAGATGATGAGACCATCA 886
 67 TGAATATGAGGCAATATTTGGAATCTTTCAGAAATGATAGATGATGAGACCATCA 126
 887 AGAATTGAGTGAACAGTAAAGTGTGATGTCCTTTGTCAGAGGAGCTGATGA 946
 127 AGAATTGAGTGAACAGTAAAGTGTGATGTCCTTTGTCAGAGGAGCTGATGA 186
 447 AGAATGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1006
 187 AGAATGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 246
 1007 TTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATA 1119
 247 TTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATA 306
 1067 AATATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATA 1119
 307 ACATCTGTAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 359
 Db 307 ACATCTGTAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 359

RESULT 14
 A1237062 517 bp mRNA linear EST 31-JAN-1999
 LOCUS E2333624 Normalized rat ovary, Bento Soares Ratus sp. cDNA clone
 DEFINITION F04243 end, mRNA sequence
 ACCESSION A1237062
 VERSION A1237062.1 GI:3830568
 KEYWORDS EST.
 SOURCE Ratus sp.
 ORGANISM Ratus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus
 1 (bases 1 to 517)
 Lee, N.H., Glodzik, A., Chandra, I., Mason, T.M., Quackenbush, J.,
 Kerlavage, A.P. and Adams, M.D.
 Rat Genome Project: Generation of a Rat EST (FEEST) Catalog & Pat
 Gene Index

JOURNAL

Unpublished (1998)
 Other ESTs: TC61253
 Contact: Lee, NH

The Institute for Genomic Research
 2712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 Seq primer: M13-21.

FEATURES

source

1..517
 Location/Qualifiers

/organism="Ratus sp."
 /db_xref="taxon:10118"
 /clone_id="F04243"
 /note="Normalized rat ovary, Bento Soares"

BASE COUNT 107 a 166 c 153 g 91 t
 ORIGIN

Query Match 15.1%; Score 306.4; DB 9; Length 517;
 Best Local Similarity 79.1%; Pred No. 12e-43;
 Matches 402; Conservative 0; Mismatches 10; Indels 5; Gaps 3;

372 GCTGAGAAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
 11 GCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 70
 433 GCGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
 71 GAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 128
 492 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 352
 129 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 188
 553 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 612
 189 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248
 613 TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 672
 249 TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 308
 673 CCGTATTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729
 309 CTTGATTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
 730 ATCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 789
 369 ACCCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 428
 790 AGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 849
 429 AGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 489
 850 CTTGATTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 877
 489 CCGTATTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516
 Db 489 CCGTATTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516

RESULT 15
 BG671440 410 bp mRNA linear EST 30-APR-2001
 LOCUS D2188F04 Rat DRG Library, Pat et al. mRNA clone D2188F04 5'
 DEFINITION mRNA sequence.
 ACCESSION BG671440
 VERSION BG671440.1 GI:13893539
 KEYWORDS EST.
 SOURCE Norway rat
 ORGANISM Ratus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (Pages 1 to 410)
AUTHORS
Xiao, H. S., Huang, Q. H., Zhang, F. X., Bao, L., Lu, Y. J., Guo, C., Yang, L.

TITLE Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain

JOURNAL,
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
MEDLINE
22056133

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Fax: 86 21-64713446
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This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park

Pudong New Area, P.R.China. Please contact with Zhang
(xu zhang1111 at 163) or Han Zhenzhen (hanzhenzhen@sh.cn)

PCR PRIMERS
FORWARD: 5'-

FORWARD: 13
BACKWARD: 77

Seq primer: 13
POLYA=No.

| PHASES | Location/Qualifiers |
|--------|---------------------|
| Source | 1. .410 |

/organism="Rattus norvegicus"
/strain="Sprague-Dawley"

